

AMENDMENTS TO THE CLAIMS

1. (Cancelled)
2. (Currently amended) The A method of claim 3 identifying candidate genes involved in systemic lupus erythematosus (SLE), comprising identifying a region of the genome adjacent to an SLE-associated marker, and selecting any gene in the region having a distance between the first nucleotide of the gene and the first nucleotide of an L1 element of less than about 200,000 base pairs as a candidate gene involved in SLE, wherein the L1 element comprises a sequence at least about 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
3. (Currently amended) A method of identifying candidate genes involved in ~~systemic lupus erythematosus (SLE)~~, comprising identifying a region of the genome adjacent to ~~a disease~~ an SLE-associated marker, and selecting any gene in the region containing an L1 element in an intronic region or in a 5' or 3' regulatory region as a candidate gene involved in SLE, wherein the L1 element comprises a sequence at least 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
- 4-18. (Cancelled)
19. (Currently amended) The method of claim 2 ~~3~~, comprising selecting any gene containing an L1 element in an intronic region as a candidate gene involved in SLE.
20. (Currently amended) The method of claim 2 ~~3~~, comprising selecting any gene containing an L1 element in a 5' regulatory region as a candidate gene involved in SLE.

30. (New) The method of claim 3, wherein the L1 element has at least about 98% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.
31. (New) The method of claim 3, wherein the L1 element has at least about 99% sequence similarity to nucleotides 1-884 of SEQ ID NO:1.
32. (New) The method of claim 3, wherein the L1 element comprises residues 1-884 of SEQ ID NO:1.
33. (New) The method of claim 3, wherein the L1 element comprises SEQ ID NO:1.
34. (New) The method of claim 3, wherein the region of the genome is within 5 million bases on either side of the SLE-associated marker.
35. (New) The method of claim 3, wherein the region of the genome is within 1.7 cM on either side of the SLE-associated marker.
36. (New) A method of identifying candidate genes involved in systemic lupus erythematosus (SLE), comprising identifying a gene containing an L1 element in an intronic region or in a 5' or 3' regulatory region, and selecting any gene within 1.7 cM of an SLE-associated marker as a candidate gene involved in SLE, wherein the L1 element comprises a sequence at least 95% similar to the sequence of nucleotides 1-884 of SEQ ID NO:1.
37. (New) The method of claim 36, wherein the L1 element comprises SEQ ID NO:1.